AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-6 (Cancelled).

7. (Previously Presented) A method of analysing a sample to determine the presence or otherwise therein of a target polynucleotide sequence, the method comprising the steps of

(a) treating the sample under hybridising conditions with

(i) a first polynucleotide probe labelled with a first exciplex partner moiety able on photoirradiation to form an exciplex with a second exciplex partner moiety, and

(ii) a second polynucleotide probe labelled with the second exciplex partner moiety, said first and second probes being adapted to bind to mutually exclusive regions of said target sequence such that said moieties are able to form said exciplex which is detectably different from the first and second moieties,

(b) effecting photoirradiation to cause exciplex formation, and

(c) detecting for formation of the exciplex to determine the presence or otherwise of the target polynucleotide sequence

wherein the sample when irradiated contains an organic solvent selected from 2,2,2-trifluoroethanol, ethylene glycol or ethylene glycol dimethyl ether.

8. (Previously Presented) A method as claimed in claim 7 wherein the sample on photoirradiation comprises an admixture of water or buffer and the solvent.

9. (Previously Presented) A method as claimed in claim 7 wherein the sample on photoirradiation comprises more than 30% by volume of the solvent.

10. (Original) A method as claimed in claim 9 wherein the sample of photoirradiation comprises more than 40% by volume of the solvent.

11. (Original) A method as claimed in claim 10 wherein the sample on photoirradiation comprises more than 50% by volume of the solvent.

12. (Original) A method as claimed in claim 11 wherein on photoirradiation the sample comprises at least 70% by volume of the solvent.

13. (Previously Presented) A method as claimed in claim 9 wherein on photoirradiation the sample comprises a maximum of 80% by volume of the solvent.

14. (Previously Presented) A method as claimed in claim 7 wherein the solvent is 2,2,2-trifluorethanol.

15. (Previously Presented) A method as claimed in claim 7 in which, prior to step (a) the sample is heated to destroy any secondary structure.

16. (Previously Presented) A method as claimed in claim 7 wherein after step (a) the sample is heated and then cooled prior to exciplex formation and detection.

17. (Original) A method as claimed in claim 16 wherein said heating after step (a) is to a temperature at which the probes, if hybridised to a target polynucleotide sequence, are denatured from the target sequence.

18. (Previously Presented) A method as claimed in claim 16 wherein said heating after step (a) is to a temperature not exceeding 90°C.

19. (Previously Presented) A method as claimed in claim 18 wherein said heating after step (a) is to a temperature not exceeding 70 °C.

20. (Previously Presented) A method as claimed in claim 19 wherein said heating after step (a) is to a temperature not exceeding 60 °C.

21. (Previously Presented) A method as claimed in claim 20 wherein said heating after step (a) is to a temperature not exceeding 50 °C.

22. (Previously Presented) A method as claimed in claim 21 wherein said heating after step (a) is to a temperature not exceeding 40 °C.

23. (Previously Presented) A method as claimed in claim 7 wherein the first polynucleotide probe is labelled at its 5' end with the first exciplex partner moiety.

24. (Previously Presented) A method as claimed in claim 7 wherein the second polynucleotide probe is labelled at its 3'-end with the second exciplex partner moiety.

25. (Previously Presented) A method as claimed in claim 7 wherein the first and second exciplex partner moieties are bonded to the first and second polynucleotide probes respectively by linkers.

26. (Previously Presented) A method as claimed in claim 7 wherein the exciplex forming partners comprise the pyrenyl group as a first partner and a second partner which comprises at least one aromatic ring.

27. (Original) A method as claimed in claim 26 wherein the second partner is a fused ring system.

28. (Original) A method as claimed in claim 27 wherein the second partner is provided with at least one electron donating group.

29. (Previously Presented) A method as claimed in claim 24 wherein one of the probes has attached thereto the 1-pyrenyl-methylamino group and the other probe has attached thereto either the 2-(N'-methyl-N'-naphthalen-1'ylamino)ethylamino group or the 2-(N'-naphthalen-1'-ylamino)ethylamino (MMN) group, said groups providing the exciplex partner moieties.

30. (Original) A method as claimed in claim 25 wherein the combination of one of the exciplex partner moieties and its associated linker group is the 2-(N'-methyl-N'-naphth-1"-ylamino)ethylamino group and the combination of the other exciplex partner moiety and its associated linker group is the pyren-1-yl-methylamino group.

31. (Currently Amended) A method as claimed in claim 7 wherein the first and second polynucleotide probes are capable of binding to the target polynucleotide sequence with the 3' end of one probe being ~~adjacent~~ proximal to the 5' end of the other probe such that there is at least one base of the polynucleotide sequence between the ~~adjacent~~ proximal 3' and 5' ends of the probes as bound to the target.

32. (Currently Amended) A method as claimed in claim 31 wherein there is one to three bases of the target between the ~~adjacent~~ proximal 3' and 5' ends of the probes as bound to the target.

33. (Previously Presented) A method as claimed in claim 7 wherein at least one of the probes has at least one base mismatch as compared to the polynucleotide sequence.

34. (Original) A method as claimed in claim 33 wherein at least one of the probes has one or two base mismatches as compared to the target polynucleotides sequence.

35. (Previously Presented) A method as claimed in claim 7 wherein the target polynucleotide sequence comprises DNA.

36. (Previously Presented) A method as claimed in claim 7 wherein the target polynucleotide sequence comprises a natural nucleic acid and/or an analogue or derivative of such a nucleic acid.

37. (Previously Presented) A method as claimed in claim 36 wherein the target nucleotide sequence comprises a nucleic acid analogue, and wherein said analogue is PNA or LNA.

38. (Previously Presented) A method as claimed in claim 7 wherein the target polynucleotide sequence comprises RNA.

39. (Original) A method as claimed in claim 38 wherein the first and second probes are DNA probes.

40. (Previously Presented) A method as claimed in claim 7 wherein the probes are DNA, RNA or analogues or derivatives of a nucleic acid.

41. (Original) A method as claimed in claim 40 wherein the probes comprise LNA or PNA.

42. (Previously Presented) A method as claimed in claim 7 wherein the probes contain a mixture of at least two of DNA, RNA and analogues or derivatives of nucleic acid in their sequence.

43. (Previously Presented) A method as claimed in claim 7 wherein the target polynucleotide sequence and the first and second polynucleotide probes are free in solution.

44. (Previously Presented) A method as claimed in claim 7 wherein at least one of the target polynucleotide sequence and/or at least one of the probes is immobilised with there being also at least one of the polynucleotide sequence and/or at least one of the probes being free in solution.

45. (Previously Presented) A method as claimed in claim 44 wherein immobilisation is on a solid substrate.

46. (Previously Presented) A method as claimed in claim 45 wherein immobilisation is on a chip, microarray, a nanoparticle or other surface.

47. (Cancelled).

48. (Previously Presented) A method as claimed in claim 18 wherein said heating after step (a) is to a temperature not exceeding 80°C.